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Figure 1

1 GGAAGTCAGCAGGCGTTGGGGAGGGGTGGCGGGGGAATAGCGGCGCAGC
51 AGCCCCAGCCCTCAGAGAGACAGCAGAAAGGAGGGAGGGGTGCTGG
101 GGGACAGCCCCCACCATTCTTACCGCTATGGGCCCCAACCTCCCACTCC
151 CACCTCCCCCTCATCGGCCGGGCTAGGACACCCCCAAATCCCGTCGCCC
201 CCTTGCCACCGACACCCCCGACAGAGACAGAGACACAGCCATCCGCCACCA
251 CCGCTGCCGAGCCTGGCTGGGAGGGGCCAGCCCCCAGGCCCCCTAC
301 CCCTCTGAGGTGCCAGA ATG GAT TTG TGG CCA GGG GCA TGG
Met Asp Leu Trp Pro Gly Ala Trp
343 ATG CTG CTG CTG CTC TTC CTG CTG CTG CTC TTC C
Met Leu Leu Leu Leu Phe Leu Leu Leu Phe L
20
10
380 TG CTG CCC ACC CTG TGG TTC TGC AGC CCC AGT GCC AAG
eu Leu Pro Thr Leu Trp Phe Cys Ser Pro Ser Ala Lys

Figure 1 (continued)

418 TAC TTC TTC AAG ATG GCC TTC TAC AAT GGC TGG ATC C
Tyr Phe Phe Lys Met Ala Phe Tyr Asn Gly Trp Ile L

40

455 TC TTC CTG GCT GTG CTC GCC ATC CCT GTG TGT GCC GTG
eu Phe Leu Ala Val Leu Ala Ile Pro Val Cys Ala Val

50

493 CGA GGA CGC AAC GTC GAG AAC ATG AAG ATC TTG CGT C
Arg Gly Arg Asn Val Glu Asn Met Lys Ile Leu Arg L

60

530 TA ATG CTG CTC CAC ATC AAA TAC CTG TAC GGG ATC CGA
eu Met Leu Leu His Ile Lys Tyr Leu Tyr Gly Ile Arg

70

80

Figure 1 (continued)

568 GTG GAG GTG CGA GGG GCT CAC CAC TTC CCT CCC TCG C
Val Glu Val Arg Gly Ala His His Phe Pro Pro Ser G

90

605 AG CCC TAT GTT GTT GTC TCC AAC CAC CAG AGC TCT CTC
In Pro Tyr Val Val Val Ser Asn His Gln Ser Ser Leu

100

643 GAT CTG CTT GGG ATG ATG GAG GTA CTG CCA GGC CGC T
Asp Leu Leu Gly Met Met Glu Val Leu Pro Gly Arg C

110

680 GT GTG CCC ATT GCC AAG CGC GAG CTA CTG TGG GCT GGC
ys Val Pro Ile Ala Lys Arg Glu Leu Leu Trp Ala Gly

120

130

Figure 1 (continued)

718 TCT GCC GGG CTG GCC TGC TGG CTG GCA GGC ATC T
Ser Ala Gly Leu Ala Cys Trp Leu Ala Gly Val Ile P

140

755 TC ATC GAC CGG AAG CGC ACG GGG GAT GCC ATC AGT GTC
he Ile Asp Arg Lys Arg Thr Gly Asp Ala Ile Ser Val

150

793 ATG TCT GAG GTC GCC CAG ACC CTG CTC ACC CAG GAC G
Met Ser Glu Val Ala Gln Thr Leu Leu Thr Gln Asp V

160

170

830 TG AGG GTC TGG GTG TTT CCT GAG GGA ACG AGA AAC CAC
al Arg Val Trp Val Phe Pro Glu Gly Thr Arg Asn His

180

Figure 1 (continued)

868 AAT GGC TCC ATG CTG CCC TTC AAA CGT GGC GCC TTC C
Asn Gly Ser Met Leu Pro Phe Lys Arg Gly Ala Phe H

190

905 AT CTT GCA GTG CAG GCC CAG GTT CCC ATT GTC CCC ATA
is Leu Ala Val Gln Ala Gln Val Pro Ile Val Pro Ile

200

943 GTC ATG TCC TCC TAC CAA GAC TTC TAC TGC AAG AAG G
Val Met Ser Ser Tyr Gln Asp Phe Tyr Cys Lys Lys G

210

220

980 AG CGT CGC TTC ACC TCG GGA CAA TGT CAG GTG CGG GTG
lu Arg Arg Phe Thr Ser Gly Gln Cys Gln Val Arg Val

230

Figure 1 (continued)

1018 CTG CCC CCA GTG CCC ACG GAA GGG CTG ACA CCA GAT G
Leu Pro Pro Val Pro Thr Glu Gly Leu Thr Pro Asp A

240

1055 AC GTC CCA GCT CTG GCT GAC AGA GTC CGG CAC TCC ATG
sp Val Pro Ala Leu Ala Asp Arg Val Arg His Ser Met

250

1093 CTC ACT GTT TTC CGG GAA ATC TCC ACT GAT GGC CGG G
Leu Thr Val Phe Arg Glu Ile Ser Thr Asp Gly Arg G

260

270

1130 GT GGT GAC TAT CTG AAG AAG CCT GGG GGC GGT GGG
ly Gly Gly Asp Tyr Leu Lys Lys Pro Gly Gly Gly 280

1168 TGA ACCCTGGCTCTGAGCTCTCCTCCCATCTGTCCCCATCTTCCTCCC
1216 CACACCTACCCACCCAGTGGGCCCTGAAGCAGGGCCAAACCCCTCTTCCTT
1266 GTCTCCCCCTCTCCCCACTTATTCTCCTCTTTGGAAATCTTCAACTTCTGAA

Figure 1 (continued)

1316 GTGAATGTGGATACAGCGCCACTCCTGCCCCCTCTTGGCCCCCATCCATGG
1366 ACTCTTGCCCTCGGTGCAGTTTCCACTCTTGACCCCCACCTCCTACTGTCT
1416 TGTCTGTGGACAGTTGCCCTCCCCCTCATCTCCAGTGACTCAGCCTACAC
1466 AAGGAGGGGAACATTCCATCCCCAGTGAGTCTCTTCCATATGTGGTCTT
1516 CTCTACCCCTCTACCCCCACATTGGCCAGTGGACTCATCCATTCTTTGGA
1566 ACAAAATCCCCCCCACCTCCAAGTCCATGGATTCAATGGACTCATCCATT
1616 TGTGAGGAGGACTTCTCGCCCTCTGGCTGGAAAGCTGATACCTGAAGCACT
1666 CCCAGGCTCATCCTGGGAGCTTTCCCTCAGCACCTTCACCTTCCCCTCCCAG
1716 TGTAGCCTCCTGTCA GTGGGGCTGGACCCCTTCTAATTCAGAGTCTCAT
1766 GCCTGCCCTTGCCCA GATGCCCAGGGTCGTGCACTCTCTGGGATACCAGT
1816 TCAGTCTCCACATTTCTGGTTTCTGTCCCCCATAGTACAGTTCTTCAGTG
1866 GACATGACCCCA CCGCCCTGCAGCCCTGCTGACCATCTCACCAGAC
1916 ACAAGGGGAAGAGCAGACATCAGGTGCTGCACCTCACTTCTGCCCCCTGG
1966 GGAGTTGGGAAAGGAACGAACCTGGCTGGAGGGGATAGGAGGGCTTTT

Figure 1 (continued)

2016 AATTATTCTTTTCTGTTGAGGCTTCCCCCTCTCTGAGCCAGTTTCA
2066 TTTCTTCCGTGGCATTAGCCACTCCCTGCCCTCTCACTCCAGACCTGTT
2116 CCCACAAC TGGGAGGTAGGCTGGGAGCAAAAGGAGAGGGTGGACCCAG
2166 TTTTGC GTGGTGGTTT TTTATTATCTGGATAACAGCAAAAAAACTG
2216 AAAATAAAGAGAGAGAGAAAAA

Figure 2

Human LPAAT	1	MDLWPGAWM-	10	20	30	40	50
Yeast LPAAT	1	MSV-IGRFLY	YLRSVL-VVL	AL-AG----	LL-LLFLLPT	LWFCSPSAKY	F-----FKMA
E.coli LPAAT	1	M-----	-----LYIF	RL-IITVIYS	ILVCVFGSIY	-----	-----G
Maize LPAAT	1	MAI-----	---PLVLVVL	PLGLLFLLSG	LIVNAIQAVL	FVTIRPFESK	-----
Human LPAAT	51	FYNGWILFLA	VLAIPVCAVR	GRNVENMKIL	RLMLLHIKYL	-YGIRVEVRG	-----
Yeast LPAAT	51	FY-----G	VIASILCTLI	GKQHLAQWIT	ARCFYHVMKL	MLGLDV---K	-----
E.coli LPAAT	51	-----	-----CLFS	PRNPKHVATF	GHMFGRLAPL	-FGLKVECRK	-----
Maize LPAAT	51	FYRRINRFLA	EL-----	-----L	WLQLVWVVDW	WAGVKVQLHA	-----
Human LPAAT	101	AHHF-PPSQ-	-PYVVVSNHQ	SSLDLLGME	VL--PGRC--	-VPI-AKREL	-----
Yeast LPAAT	101	VUGE-ENLAK	KPYIMIANHQ	STLDIFMLGR	IF--PPGCT-	---VTAKKSL	-----
E.coli LPAAT	101	PTDA-ESYG-	-NAIYIANHQ	NNYDMVTASN	IVQ-PP----	TVTV-GKKSL	-----
Maize LPAAT	101	DEETYRSMGK	EHALIISNHR	SDIDWL-IGW	ILAQRSGCLG	STLAVMKKSS	-----
Human LPAAT	151	LWAGSAGLAC	W---LAGVIF	IDRKRTGDAI	SVMSEVAQTL	LTQDVRVWV-	-----
Yeast LPAAT	151	KYVPFLG---	WFMA LSGTYF	LDRSKRQEA I	DTLNKGLENV	KKNKRALWV-	-----
E.coli LPAAT	151	LWIPFFGQLY	W---LTGNLL	IDRNNRTKAH	GTIAEVVNHF	KKRRISIW-	-----
Maize LPAAT	151	KFLPVI GWSM	WF---AEYLF	LEERS-WAKDE	KTLKWGLQRL	KDFPRPFWLA	-----
Human LPAAT	201	-FPEGTRNHN	GS-----	-----	MLPFKRGAFH	LAVQAQVPV	-----
Yeast LPAAT	201	-FPEGTRSYT	SEL-----	-----T	MLPFKKGA FH	LAQQGKIPIV	-----
E.coli LPAAT	201	-FPEGTRSRG	RGL-----	-----	-LPFKTGAFH	AAIAAGVPII	-----
Maize LPAAT	201	LFVEGTRFTP	AKLLAAQEYA	ASQGLPAPRN	VLIPRTKGFV	SAVSIMRDFV	-----

Figure 2 (continued)

Human LPAAT	251	PIVMSSYQDF	YCKKERRFTS	GQCQVRVLPP	VPTEGLTPDD	VPALADR---
Yeast LPAAT	251	PVVVSNTSTL	VSPKYGVFNR	GCMIVRILKP	ISTENLTCKD	IGEFAEK---
E.coli LPAAT	251	PVCVSTTSNK	I--NLNRLHN	GLVIVEMLPP	IDVSQYGKDQ	VRELAH---
Maize LPAAT	251	PAIYDTT--V	IVPKDSPQPT	MLRILKGQSS	VIHVRMKRHA	MSEMPKSD
		260	270	280	290	300
Human LPAAT	301	-----	VRHSMITV-F	REISTDGRGG	GDYLKKPGGG	G*.....
Yeast LPAAT	301	-----	VRDQMVDL	KEIGYSPAIN	DTTLPQ---	-----
E.coli LPAAT	301	-----	CRSIMEQK-I	AELDKVAE-	----REAAKG	V*.....
Maize LPAAT	301	VSKWCKDIFV	AKDALLDKHL	ATGTFDEEIR	PIGRPVKSLL	VTLFWSCLLL
		310	320	330	340	350
Human LPAAT	351
Yeast LPAAT	351	--AIEY--A	AL-----Q	HDKKVNKKIK	NEPVPSVSIS	NDVNTHNEGS
E.coli LPAAT	351
Maize LPAAT	351	FGAIEFFKWT	QLLSTWRGVA	FTAAGMALVT	GVMHVFIMFS	QA-----ERS
		360	370	380	390	400
Human LPAAT	401
Yeast LPAAT	401	S-----V	KKMH*
E.coli LPAAT	401
Maize LPAAT	401	SSARAARNRV	KKE*
		410	420	430	440	450

Figure 3

10	20	30	40	50	60
GGAGCGAGCT	GGCGGCGCCG	TCGGGCGCCG	GGCCGGGCCA	TGGAGCTGTG	GCCGTGTCTG
70	80	90	100	110	120
GCCGCGGCGC	TGCTGTGTGCT	GCTGCTGCTG	GTGCAGCTGA	GCCGCGCGGC	CGAGTTCTAC
130	140	150	160	170	180
GCCAAGGTCTG	CCCTGTACTG	CGCGCTGTGC	TTCACGGTGT	CCGCCGTGGC	CTCGCTCGTC
190	200	210	220	230	240
TGCCTGCTGT	GCCACGGCGG	CCGGACGGTG	GAGAACATGA	GCATCATCGG	CTGGTTCTGTG
250	260	270	280	290	300
CGAAGCTTCA	AGTACTTTTA	CGGGCTCCGC	TTCGAGGTGC	GGGACCCGCG	CAGGCTGCAG
310	320	330	340	350	360
GAGGCCCGTC	CCTGTGTCAT	CGTCTCCAAC	CACCAGAGCA	TCCTGGACAT	GATGGGCCCTC
370	380	390	400	410	420
ATGGAGGTCC	TTCCGGAGCG	CTGCGTGCAG	ATCGCCAAGC	GGGAGCTGCT	CTTCCCTGGGG
430	440	450	460	470	480
CCCGTGGGCC	TCATCATGTA	CCTCGGGGGC	GTCTTCTTCA	TCAACCGGCA	GCGCTCTAGC
490	500	510	520	530	540
ACTGCCATGA	CAGTGATGGC	CGACCTGGGC	GAGCGCATGG	TCAGGGAGAA	CCTCAAAGTG

Figure 3 (continued)

550	560	570	580	590	600
TGGATCTATC	CCGAGGGTAC	TCGCAACGAC	AATGGGGACC	TGCTGCCCTTT	TAAGAAGGGC
610	620	630	640	650	660
GCCTTCTACC	TGGCAGTCCA	GGCACAGGTG	CCCATCGTCC	CCGTGGTGTA	CTCTTCCTTC
670	680	690	700	710	720
TCCTCCTTCT	ACAACACCAA	GAAGAAGTTC	TTCACTTCAG	GAACAGTCAC	AGTGCAGGTG
730	740	750	760	770	780
CTGGAAGCCA	TCCCCACCAG	CGGCCTCACT	GCGGCGGACG	TCCCTGCGCT	CGTGGACACC
790	800	810	820	830	840
TGCCACCCGG	CCATGAGGAC	CACCTTCCTC	CACATCTCCA	AGACCCCCCA	GGAGAACGGG
850	860	870	880	890	900
GCCACTGCGG	GGTCTGGCGT	GCAGCCCGGC	CAGTAGCCCA	GACCACGGCA	GGGCATGACC
910	920	930	940	950	960
TGGGGAGGGC	AGGTGGAAGC	CGATGGCTGG	AGGATGGGCA	GAGGGGACTC	CTCCCCGGCTT
970	980	990	1000	1010	1020
CCAAATACCA	CTCTGTCCGG	CTCCCCCAGC	TCTCACTCAG	CCCGGGAAGC	AGGAAGCCCC
1030	1040	1050	1060	1070	1080
TTCTGTCACT	GGTCTCAGAC	ACAGGCCCCCT	GGTGTCCCTT	GCAGGGGGCT	CAGCTGGACC

Figure 3 (continued)

1090	1100	1110	1120	1130	1140
CTCCCCGGGC	TCGAGGGCAG	GGA CTGCGC	CCACGGCACC	TCTGGGNGCT	GGGNTGATAA
1150	1160	1170	1180	1190	1200
AGATGAGGCT	TGCGGCTGTG	GCCCCGCTGGT	GGGCTGAGCC	ACAAGGCCCC	CGATGGCCCA
1210	1220	1230	1240	1250	1260
GGAGCAGATG	GGAGGACCCC	GAGGCCAGGA	GTCCCAGACT	CACGCACCCCT	GGGCCACAGG
1270	1280	1290	1300	1310	1320
GAGCCGGGAA	TCGGGGCCTG	CTGCTCCTGC	TGGCCTGAAG	AATCTGTGGG	GTCAGCACTG
1330	1340	1350	1360	1370	1380
TACTCCGTTG	CTGTTTTTTT	ATAAACACAC	TCTTGGA AAA	AAAAAAAAAA	AAAAAAAAAA
1390	1400	1410	1420	1430	1440
AAA.....

Figure 4

10	20	30	40	50
GGAGCGAGCTGGCGCGCGCGTCTGGCGCGCGCGCGGCC	ATG	GAG	CTG	TGG
	Met	Glu	Leu	Trp
				Pro
60	70	80	90	
TGT CTG GCC GCG GCG CTG CTG CTG TTG CTG CTG CTG	CTG	CTG	CTG	CAG
Cys Leu Ala Ala Ala Leu Leu Leu Leu Leu Leu	Val	Gln	Leu	
	10	20		
100	110	120	130	140
AGC CGC GCG GCC GAG TTC TAC GCC AAG GTC GCC	CTG	TAC	TGC	GCG
Ser Arg Ala Ala Glu Phe Tyr Ala Lys Val Ala	Leu	Tyr	Cys	Ala
	30			
150	160	170	180	
CTG TGC TTC ACG GTG TCC GCC GTG GCC TCG CTC	GTC	TGC	CTG	CTG
Leu Cys Phe Thr Val Ser Ala Val Ala Ser Leu	Val	Cys	Leu	Leu
	40			50
190	200	210	220	230
TGC CAC GGC GGC CCG ACG GTG GAG AAC ATG AGC	ATC	ATC	ATC	GGC
Cys His Gly Gly Arg Thr Val Glu Asn Met Ser	Ile	Ile	Gly	Trp
	60			

Figure 4 (continued)

240	TTC GTG CGA AGC TTC AAG TAC TTT TAC GGG CTC	270	CGC TTC GAG GTG
	Phe Val Arg Ser Phe Lys Tyr Phe Tyr Gly Leu Arg		Phe Glu Val
	70		80
280	290	300	310
	CGG GAC CCG CGC AGG CTG CAG GAG GCC CGT CCC		TGT GTC ATC GTC
	Arg Asp Pro Arg Arg Leu Gln Glu Ala Arg Pro		Cys Val Ile Val
		90	
330	340	350	360
	TCC AAC CAC CAG AGC ATC CTG GAC ATG ATG GGC CTC		ATG GAG GTC
	Ser Asn His Gln Ser Ile Leu Asp Met Met Gly Leu		Met Glu Val
	100		110
370	380	390	400
	CTT CCG GAG CGC TGC GTG CAG ATC GCC AAG CCG GAG		CTC CTC TTC
	Leu Pro Glu Arg Cys Val Gln Ile Ala Lys Arg Glu Leu		Phe
		120	
420	430	440	450
	CTG GGG CCC GTG GGC CTC ATC ATG TAC CTC GGG GGC		GTC TTC TTC
	Leu Gly Pro Val Gly Leu Ile Met Tyr Leu Gly Val		Phe
	130		140
460	470	480	490
	ATC AAC CCG CAG CGC TCT AGC ACT GCC ATG ACA GTG		ATG GCC GAC
	Ile Asn Arg Gln Arg Ser Ser Thr Ala Met Thr Val		Met Ala Asp
		150	

Figure 4 (continued)

510	520	530	540	
CTG GGC GAG CGC ATG GTC AGG GAG AAC CTC AAA GTG TGG ATC TAT				
Leu Gly Glu Arg Met Val Arg Glu Asn Leu Lys Val Trp Ile Tyr				170
160				
550	560	570	580	590
CCC GAG GGT ACT CGC AAC GAC AAT GGG GAC CTG CTG CCT TTT AAG				
Pro Glu Gly Thr Arg Asn Asp Asn Gly Asp Leu Leu Pro Phe Lys				
				180
600	610	620	630	
AAG GGC GCC TTC TAC CTG GCA GTC CAG GCA CAG GTG CCC ATC GTC				
Lys Gly Ala Phe Tyr Leu Ala Val Gln Ala Gln Val Pro Ile Val				200
190				
640	650	660	670	680
CCC GTG GTG TAC TCT TCC TTC TCC TCC TTC TAC AAC ACC AAG AAG				
Pro Val Val Tyr Ser Ser Phe Ser Ser Phe Tyr Asn Thr Lys Lys				
				210
690	700	710	720	
AAG TTC TTC ACT TCA GGA ACA GTC ACA GTG CAG GTG CTG GAA GCC				
Lys Phe Phe Thr Ser Gly Thr Val Thr Val Gln Val Leu Glu Ala				230
				220

Figure 4 (continued)

[illegible]

Figure 4 (continued)

1110	1120	1130	1140	1150	1160
	GGACTCGGCCACGGCACCTCTGGGNGCTGGNTGATAAAGATGAGGCTTGCGGCTGTG				
1170	1180	1190	1200	1210	1220
	GCCCGCTGGTGGCTGAGCCACAAGGCCCCCGATGGCCAGGAGCAGATGGGAGGACCCC				
1230	1240	1250	1260	1270	1280
	GAGGCCAGGAGTCCAGACTCACGCACCCCTGGGCCACAGGAGCCGGGAATCGGGGCTG				
1290	1300	1310	1320	1330	1340
	CTGCTCCTGCTGGCCTGAAGAACTCTGTGGGTCAGCACTGTACTCCGTTGCTGTTTTTT				
1350	1360	1370	1380		
	ATAAACACACTCTTGGAATAAAAAAAAAAAAAAAAAAAAAA				

Figure 5
Alignment of LPAAT Sequences.

Human LPAAT- β	1	10	20	30	40	50
Human LPAAT- α	1	10	20	30	40	50
Yeast LPAAT	1	10	20	30	40	50
E.coli LPAAT	1	10	20	30	40	50
H.influenzae	1	10	20	30	40	50
S.typhimurii	1	10	20	30	40	50
L.douglasi	1	10	20	30	40	50
C. nificera	1	10	20	30	40	50
Human LPAAT- β	51	60	70	80	90	100
Human LPAAT- α	51	60	70	80	90	100
Yeast LPAAT	51	60	70	80	90	100
E.coli LPAAT	51	60	70	80	90	100
H.influenzae	51	60	70	80	90	100
S.typhimurii	51	60	70	80	90	100
L.douglasi	51	60	70	80	90	100
C. nificera	51	60	70	80	90	100

Figure 5 (continued)

	110	120	130	140	150
Human LPAAT- β	101 <u>GW</u> <u>FV</u> <u>RS</u> <u>FK</u> <u>Y</u> -	-- <u>FY</u> <u>GL</u> <u>RF</u> <u>EV</u>	<u>RD</u> <u>PR</u> <u>RL</u> <u>Q</u> <u>EAR</u>	<u>PC</u> <u>VI</u> <u>VS</u> <u>NH</u> <u>Q</u> <u>S</u>	<u>I</u> <u>LD</u> <u>MM</u> <u>GL</u> <u>ME</u> <u>V</u>
Human LPAAT- α	101 <u>RL</u> <u>ML</u> <u>LI</u> <u>HI</u> <u>KY</u> -	-- <u>LY</u> <u>G</u> <u>IR</u> <u>VE</u> <u>V</u>	<u>RG</u> <u>AH</u> <u>FP</u> <u>PS</u> <u>Q</u>	<u>PY</u> <u>VV</u> <u>VS</u> <u>NH</u> <u>Q</u> <u>S</u>	<u>S</u> <u>LD</u> <u>IL</u> <u>GM</u> <u>ME</u> <u>V</u>
Yeast LPAAT	101 <u>CF</u> <u>Y</u> - <u>HV</u> <u>MK</u> <u>L</u> -	-- <u>ML</u> <u>GL</u> <u>DK</u> <u>V</u>	<u>VG</u> <u>EE</u> <u>N</u> <u>AK</u> - <u>K</u>	<u>PY</u> <u>IM</u> <u>IA</u> <u>NH</u> <u>Q</u> <u>S</u>	<u>T</u> <u>LD</u> <u>IF</u> <u>ML</u> <u>GR</u> <u>I</u>
E.coli LPAAT	101 <u>GH</u> <u>MF</u> <u>GR</u> <u>L</u> ---	<u>AP</u> <u>LF</u> <u>GL</u> <u>K</u> <u>VE</u> <u>C</u>	<u>RK</u> <u>PT</u> <u>DA</u> <u>ES</u> <u>Y</u> <u>G</u>	<u>NA</u> <u>IY</u> <u>IA</u> <u>NH</u> <u>Q</u> <u>N</u>	<u>NY</u> <u>DM</u> <u>VT</u> <u>AS</u> <u>NI</u>
H.influenzae	101 <u>AR</u> <u>WF</u> <u>GR</u> <u>L</u> - <u>FT</u>	<u>YPL</u> <u>FL</u> <u>GL</u> <u>K</u> <u>VE</u> <u>H</u>	<u>RI</u> <u>PQ</u> <u>DQ</u> <u>K</u> <u>Q</u> <u>IS</u>	<u>RA</u> <u>IY</u> <u>IG</u> <u>NH</u> <u>Q</u> <u>N</u>	<u>NY</u> <u>DM</u> <u>VT</u> <u>IS</u> <u>YM</u>
S.typhimurium	101 <u>GH</u> <u>MF</u> <u>GR</u> <u>L</u> - <u>FT</u>	<u>AP</u> <u>LF</u> <u>GL</u> <u>K</u> <u>VE</u> <u>C</u>	<u>RK</u> <u>PA</u> <u>DA</u> <u>EN</u> <u>Y</u> <u>G</u>	<u>NA</u> <u>IY</u> <u>IA</u> <u>NH</u> <u>Q</u> <u>N</u>	<u>NY</u> <u>DM</u> <u>VT</u> <u>AA</u> <u>NI</u>
L.douglassi	101 <u>GH</u> <u>II</u> <u>IG</u> <u>LV</u> --	<u>IT</u> <u>WY</u> <u>GI</u> <u>PI</u> <u>KI</u>	<u>QG</u> <u>SE</u> <u>HI</u> <u>KK</u> <u>RA</u>	<u>IFT</u> <u>YI</u> <u>SN</u> <u>HA</u> <u>S</u>	<u>PI</u> <u>DA</u> <u>FF</u> <u>VM</u> <u>L</u>
C. nucifera	101 <u>GH</u> <u>VT</u> <u>GR</u> <u>ML</u> <u>FT</u>	<u>MW</u> <u>IL</u> <u>GN</u> <u>PT</u> <u>TI</u>	<u>EG</u> <u>SE</u> <u>FS</u> <u>NT</u> <u>RA</u>	<u>I</u> -- <u>YI</u> <u>CN</u> <u>HA</u> <u>S</u>	<u>LV</u> <u>DI</u> <u>FI</u> <u>LM</u> <u>WL</u>
Human LPAAT- β	151 <u>LP</u> <u>ER</u> <u>CV</u> <u>Q</u> <u>IAK</u>	<u>RE</u> <u>LL</u> <u>FL</u> <u>GP</u> <u>V</u> -	-- <u>GL</u> <u>IM</u> <u>YL</u> <u>GV</u>	<u>FF</u> <u>IN</u> <u>RQ</u> <u>RS</u> <u>ST</u>	<u>AM</u> <u>T</u> -- <u>VM</u> <u>AD</u> <u>L</u>
Human LPAAT- α	151 <u>LP</u> <u>GR</u> <u>CV</u> <u>PIAK</u>	<u>RE</u> <u>LL</u> <u>W</u> <u>AG</u> <u>SA</u> -	-- <u>GL</u> <u>AC</u> <u>WL</u> <u>AG</u> <u>V</u>	<u>IF</u> <u>ID</u> <u>RK</u> <u>RT</u> <u>GD</u>	<u>AI</u> <u>S</u> -- <u>VM</u> <u>SE</u> <u>V</u>
Yeast LPAAT	151 <u>FP</u> <u>PG</u> <u>CT</u> <u>VTAK</u>	<u>KS</u> <u>LV</u> <u>PP</u> <u>FL</u> -	-- <u>GW</u> <u>FA</u> <u>LS</u> <u>GT</u>	<u>YF</u> <u>LD</u> <u>RS</u> <u>KR</u> <u>QE</u>	<u>AI</u> <u>D</u> -- <u>T</u> <u>IN</u> <u>KG</u>
E.coli LPAAT	151 <u>VQ</u> <u>PT</u> <u>VT</u> <u>TVGK</u>	<u>KS</u> <u>LV</u> <u>W</u> <u>IP</u> <u>FF</u> -	-- <u>GQ</u> <u>LY</u> <u>WL</u> <u>TG</u> <u>N</u>	<u>LL</u> <u>ID</u> <u>RN</u> <u>NR</u> <u>TK</u>	<u>AH</u> <u>G</u> -- <u>T</u> <u>IA</u> <u>EV</u>
H.influenzae	151 <u>VQ</u> <u>PR</u> <u>TV</u> <u>SVGK</u>	<u>KS</u> <u>LV</u> <u>W</u> <u>IP</u> <u>FF</u> <u>FF</u>	<u>TG</u> <u>IL</u> <u>Y</u> <u>W</u> <u>VT</u> <u>GN</u>	<u>IF</u> <u>LD</u> <u>RE</u> <u>NR</u> <u>TK</u>	<u>AH</u> <u>N</u> -- <u>T</u> <u>MS</u> <u>QL</u>
S.typhimurium	151 <u>VQ</u> <u>PT</u> <u>VT</u> <u>TVGK</u>	<u>KS</u> <u>LV</u> <u>W</u> <u>IP</u> <u>FF</u> <u>FF</u>	<u>TG</u> <u>Q</u> <u>LY</u> <u>W</u> <u>LT</u> <u>GN</u>	<u>LL</u> <u>ID</u> <u>RN</u> <u>NR</u> <u>AK</u>	<u>AH</u> <u>S</u> -- <u>T</u> <u>IA</u> <u>AV</u>
L.douglassi	151 <u>AP</u> <u>IG</u> <u>TV</u> <u>GVAK</u>	<u>KE</u> <u>VI</u> <u>W</u> <u>Y</u> <u>P</u> <u>IL</u> <u>G</u>	<u>Q</u> -- <u>LY</u> <u>T</u> <u>LA</u> <u>H</u>	<u>IR</u> <u>ID</u> <u>RS</u> <u>NP</u> <u>AA</u>	<u>AI</u> <u>Q</u> <u>S</u> <u>FM</u> <u>KEA</u>
C. nucifera	151 <u>IP</u> <u>KG</u> <u>TV</u> <u>TJAK</u>	<u>KE</u> <u>II</u> <u>W</u> <u>Y</u> <u>P</u> <u>IL</u> <u>FG</u>	<u>Q</u> <u>PT</u> <u>LY</u> <u>V</u> <u>LA</u> <u>NH</u>	<u>Q</u> <u>R</u> <u>ID</u> <u>RS</u> <u>NP</u> <u>SA</u>	<u>AI</u> <u>ES</u> -- <u>I</u> <u>KE</u> <u>V</u>

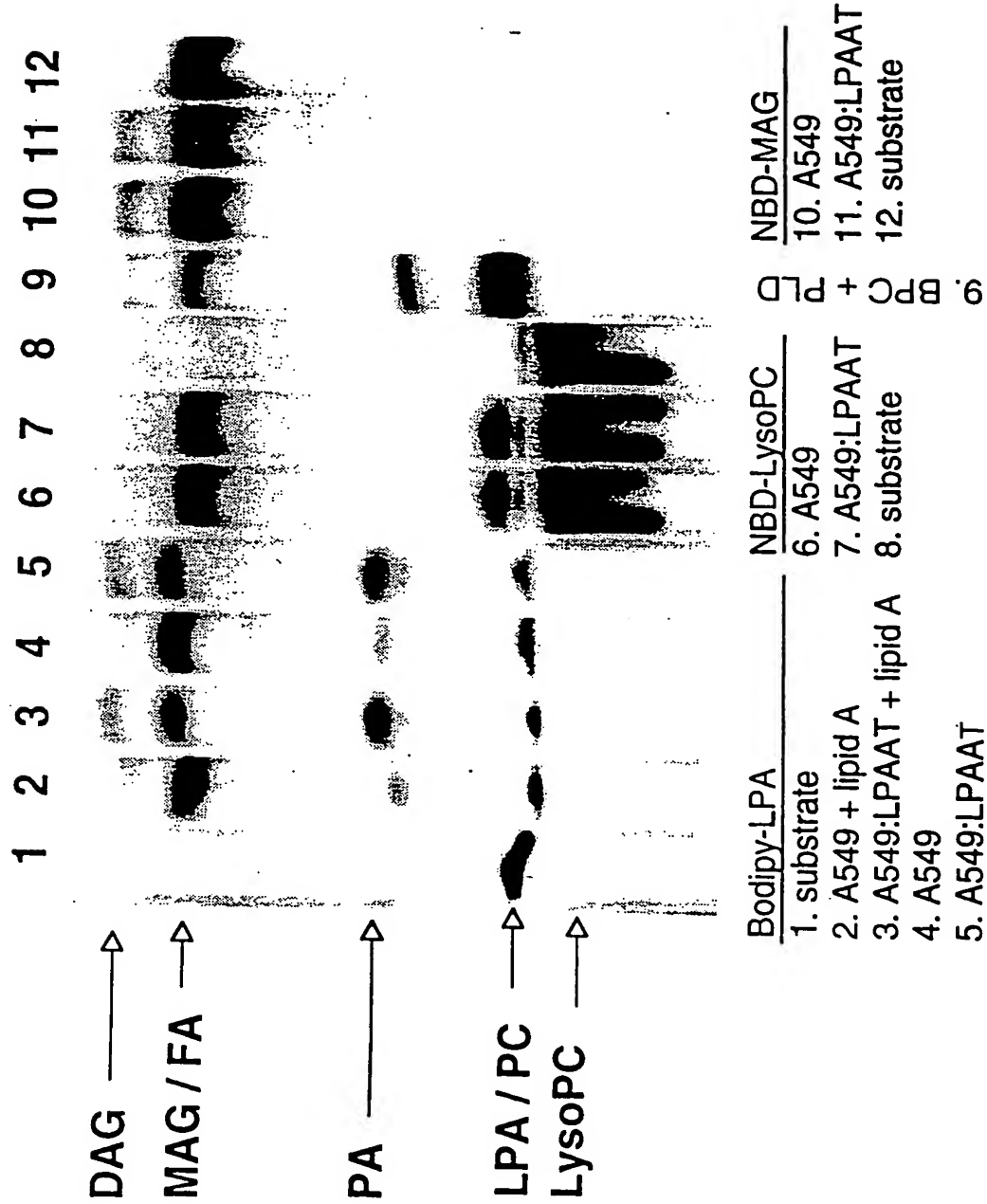
Figure 5 (continued)

Human LPAAT-β	201	<u>GERMREN</u> <u>LK</u>	<u>VWI</u> <u>Y</u> <u>PEGTRN</u>	<u>DNGDL</u> — <u>LPF</u>	<u>KKGAF</u> <u>YL</u> — <u>A</u>	<u>VQAQVPI</u> <u>VPV</u>
Human LPAAT-α	201	<u>AQTLLTQDVR</u>	<u>VWVF</u> <u>PEGTRN</u>	<u>HNGSM</u> — <u>LPF</u>	<u>KRGAF</u> <u>HL</u> — <u>A</u>	<u>VQAQVPI</u> <u>VP</u> <u>I</u>
Yeast LPAAT	201	<u>LENVKKNKRA</u>	<u>LWVF</u> <u>PEGTRS</u>	<u>YISEL</u> <u>TM</u> <u>LPF</u>	<u>KKGAF</u> <u>HL</u> — <u>A</u>	<u>QQQKI</u> <u>PI</u> <u>VPV</u>
E.coli LPAAT	201	<u>VNHFKRR</u> <u>IS</u>	<u>IWMF</u> <u>PEGTRS</u>	<u>RGRGL</u> — <u>LPF</u>	<u>KTGAF</u> — <u>HAA</u>	<u>IAAGVPI</u> <u>IPV</u>
H.influenzae	201	<u>ARRIN</u> <u>EDNLS</u>	<u>IWMF</u> <u>PEGTRN</u>	<u>RGRGL</u> — <u>LPF</u>	<u>KTGAF</u> <u>TF</u> <u>HAA</u>	<u>ISAGVPI</u> <u>IPV</u>
S.typhimurii	201	<u>VNHFKRR</u> <u>IS</u>	<u>IWMF</u> <u>PEGTRS</u>	<u>RGRGL</u> — <u>LPF</u>	<u>KTGAF</u> <u>TF</u> <u>HAA</u>	<u>IAAGVPI</u> <u>IPV</u>
L.douglassi	201	<u>VRVIT</u> <u>TEKNLS</u>	<u>LIMF</u> <u>PEGTRS</u>	<u>GDGRL</u> — <u>LPF</u>	<u>KKGFV</u> <u>HL</u> — <u>A</u>	<u>LQSHL</u> <u>PI</u> <u>VPM</u>
C. nucifera	201	<u>ARAWK</u> <u>KNLS</u>	<u>LIIF</u> <u>PEGTRS</u>	<u>KTGRL</u> — <u>LPF</u>	<u>KKGFI</u> <u>HFT</u> <u>IA</u>	<u>LQTRL</u> <u>PI</u> <u>VPM</u>
Human LPAAT-β	251	<u>VYSSF</u> <u>SS</u> — <u>F</u>	<u>YNT</u> <u>KKF</u> <u>FTS</u>	<u>GIVIVQV</u> <u>LEA</u>	<u>IPTSGLT</u> <u>AAD</u>	<u>VPAL</u> <u>VD</u> <u>ICHR</u>
Human LPAAT-α	251	<u>VMSS</u> <u>YQD</u> — <u>F</u>	<u>YCKK</u> <u>ERR</u> <u>FTS</u>	<u>GQQV</u> <u>RV</u> <u>LPP</u>	<u>VPT</u> <u>EGLT</u> <u>PDD</u>	<u>VPALAD</u> <u>IV</u> <u>RH</u>
Yeast LPAAT	251	<u>VVSNT</u> <u>ST</u> — <u>L</u>	<u>VSPK</u> <u>YGV</u> <u>FNR</u>	<u>GMI</u> <u>VR</u> <u>IL</u> <u>KP</u>	<u>IST</u> <u>EN</u> <u>LT</u> <u>KDK</u>	<u>IG</u> <u>EFA</u> <u>EK</u> <u>VRD</u>
E.coli LPAAT	251	<u>CVS</u> <u>TTS</u> — <u>---</u>	<u>NK</u> <u>IN</u> <u>LN</u> <u>RI</u> <u>HN</u>	<u>GLV</u> <u>IV</u> <u>E</u> <u>M</u> <u>LPP</u>	<u>ID</u> <u>V</u> <u>SQ</u> <u>G</u> <u>KDQ</u>	<u>VRE</u> <u>LAA</u> <u>HCR</u> —
H.influenzae	251	<u>VCS</u> <u>STH</u> — <u>---</u>	<u>NK</u> <u>IN</u> <u>LN</u> <u>R</u> <u>W</u> <u>DN</u>	<u>GK</u> <u>VI</u> <u>CE</u> <u>I</u> <u>M</u> <u>DP</u>	<u>ID</u> <u>V</u> <u>S</u> <u>G</u> <u>Y</u> <u>T</u> <u>KDN</u>	<u>VRD</u> <u>LAA</u> <u>YCH</u> <u>F</u>
S.typhimurii	251	<u>CVS</u> <u>NIS</u> — <u>---</u>	<u>NK</u> <u>VN</u> <u>LN</u> <u>R</u> <u>I</u> <u>NN</u>	<u>GLV</u> <u>IV</u> <u>E</u> <u>M</u> <u>LPP</u>	<u>VD</u> <u>V</u> <u>S</u> <u>E</u> <u>X</u> <u>G</u> <u>KDQ</u>	<u>VRE</u> <u>LAA</u> <u>HCR</u> <u>F</u>
L.douglassi	251	<u>I</u> <u>LT</u> <u>GTH</u> <u>LAW</u> <u>F</u>	<u>TR</u> <u>K</u> <u>G</u> <u>I</u> <u>F</u> <u>R</u> <u>VRP</u>	<u>VP</u> <u>I</u> <u>T</u> <u>V</u> <u>K</u> <u>Y</u> <u>LPP</u>	<u>INT</u> <u>DD</u> <u>WT</u> <u>V</u> <u>DK</u>	<u>IDD</u> <u>V</u> <u>V</u> <u>K</u> <u>MI</u> <u>HD</u>
C. nucifera	251	<u>VL</u> <u>T</u> <u>GTH</u> <u>LAW</u> —	<u>-R</u> <u>K</u> <u>N</u> <u>S</u> <u>L</u> <u>R</u> <u>VRP</u>	<u>AP</u> <u>I</u> <u>T</u> <u>V</u> <u>K</u> <u>Y</u> <u>F</u> <u>S</u> <u>P</u>	<u>I</u> <u>K</u> <u>T</u> <u>DD</u> <u>W</u> <u>E</u> <u>E</u> <u>K</u>	<u>IN</u> <u>H</u> <u>Y</u> <u>V</u> <u>E</u> <u>M</u> <u>I</u> <u>H</u> <u>F</u>

Figure 5 (continued)

	310	320	330	340	350
Human LPAAT- β	301 <u>AMRTTFIHIS</u>	<u>KTPQENGATA</u>	<u>GSGVQPAQ*</u>	-----	-----
Human LPAAT- α	301 <u>SMLT</u> <u>VFREIS</u>	<u>TDGRGGDYL</u>	<u>KKPGGG*</u>	-----	-----
Yeast LPAAT	301 <u>QMVDILKEIG</u>	<u>YSPAINDTTL</u>	<u>PPQAIEYAAL</u>	<u>QHDKKVNKKI</u>	<u>KNEPVPSVSI</u>
E.coli LPAAT	301 <u>-SIMEQKIAE</u>	<u>LDKEVA</u>	<u>-ER EAAGKV*</u>	-----	-----
H.influenzae	301 <u>TDLMEKRIAE</u>	<u>LDEEIA</u>	-----	<u>KGN*</u>	-----
S.typhimurii	301 <u>TALMEQKIAE</u>	<u>LDKEVA</u>	<u>-ER EATCKV*</u>	-----	-----
L.douglassi	301 <u>IYVRNLPASQ</u>	<u>KPIGS</u>	<u>-TNR -S-K*</u>	-----	-----
C. nucifera	301 <u>TALYVDHLPE</u>	<u>SQKPLVSKGR</u>	<u>DASGRNS*</u>	-----	-----
	360	370	380	390	
Human LPAAT- β	351 -----
Human LPAAT- α	351 -----
Yeast LPAAT	351 <u>SNDVNTHNEG</u>	<u>SSVKKMH*</u>
E.coli LPAAT	351 -----
H.influenzae	351 -----
S.typhimurii	351 -----
L.douglassi	351 -----
C. nucifera	351 -----

Figure 6



TLC Analysis of Acyltransferase Activity

**Induction of TNF in A549 LPAAT or A549
cells stimulated with mTNF and IL-1**

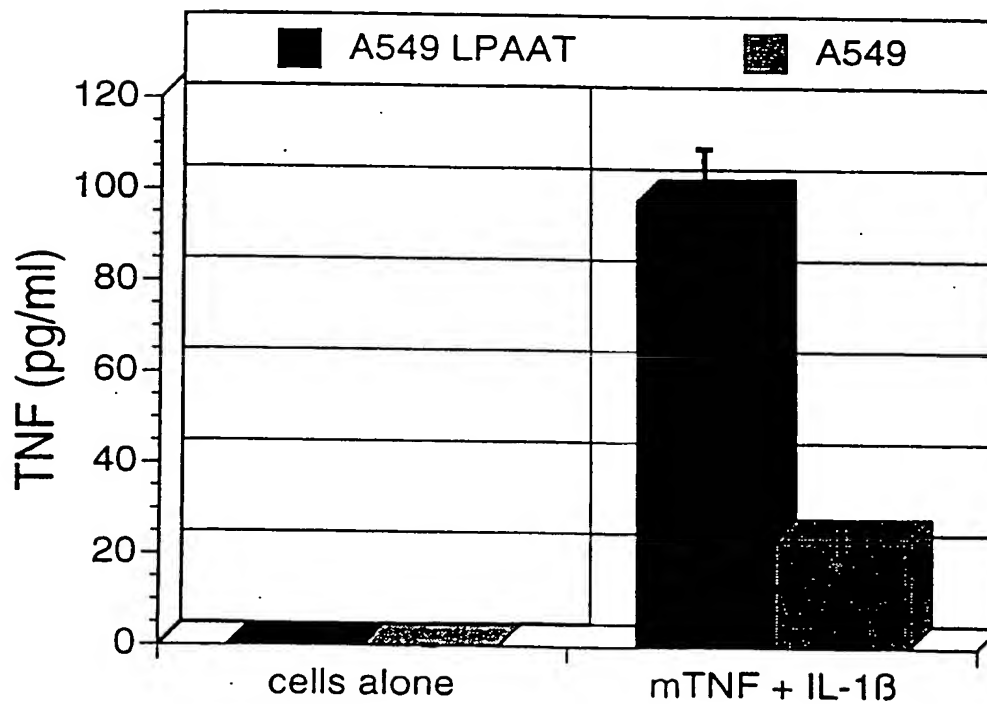


Figure 7

**Induction of IL-6 in A549 LPAAT or A549
cells stimulated with mTNF and IL-1**

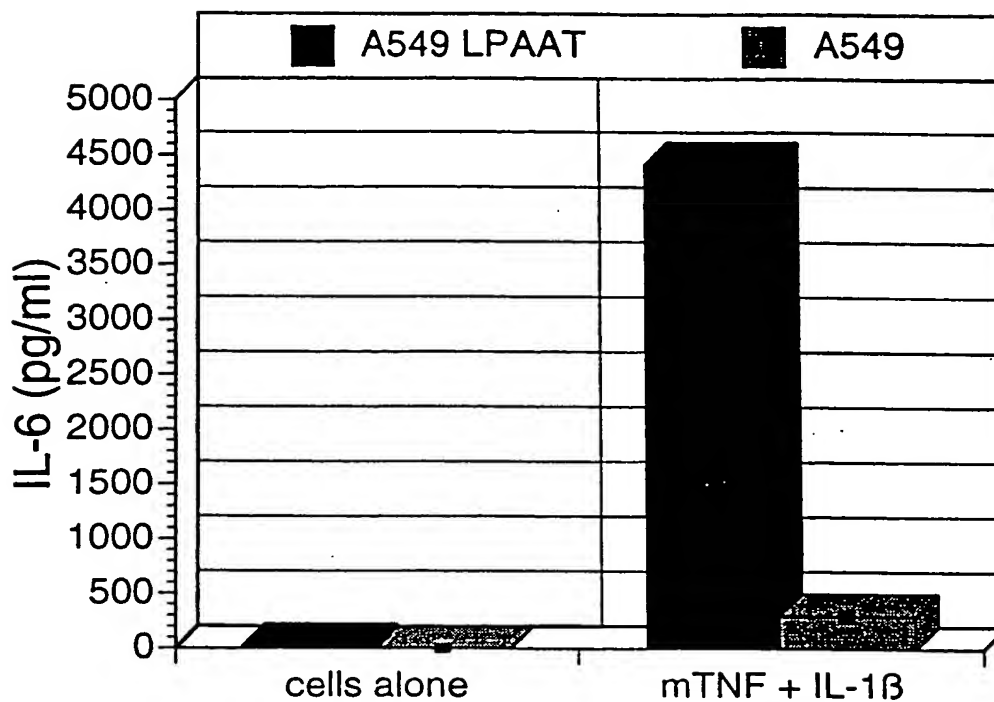


Figure 8

Title: METHOD OF SCREENING
COMPOUNDS THAT INHIBIT
LYSOPHOSPHATIDIC ACID
ACYLTRANSFERASE
Inventors: David W. LEUNG et al.
Docket No.: 077319-0383

Figure 9 Translated sequence of human LPAAT-yl

TCTATGAAACCAACATACATGGCGTTTGCATCACAGTTGGAGTCAGATGTGAGCCCGGAG	60
GGCAGGTGTCTGGCTTGTCCACCCGGAAGCCCTGAGGGCAGCTGTTCCCACTGGCTCTGC	120
TGACCTTGTGCCTTGGACGGCTGTCCTCAGCGAGGGGCGGTGCACCCGCTCCTGAGCAGC	180
GCC ATG GGC CTG CTG GCC TTC CTG AAG ACC CAG TTC GTG CTG CAC	225
Met Gly Leu Leu Ala Phe Leu Lys Thr Gln Phe Val Leu His	
5 10	
CTG CTG GTC GGC TTT GTC TTC GTG GTG AGT GGT CTG GTC ATC AAC	270
Leu Leu Val Gly Phe Val Phe Val Val Ser Gly Leu Val Ile Asn	
15 20 25	
TTC GTC CAG CTG TGC ACG CTG GCG CTC TGG CCG GTC AGC AAG CAG	315
Phe Val Gln Leu Cys Thr Leu Ala Leu Trp Pro Val Ser Lys Gln	
30 35 40	
CTC TAC CGC CGC CTC AAC TGC CGC CTC GCA TAC TCA CTC TGG AGC	360
Leu Tyr Arg Arg Leu Asn Cys Arg Leu Ala Tyr Ser Leu Trp Ser	
45 50 55	
CAA CTG GTC ATG CTG CTG GAG TGG TGG TCC TGC ACG GAG TGT ACA	405
Gln Leu Val Met Leu Leu Glu Trp Trp Ser Cys Thr Glu Cys Thr	
60 65 70	
CTG TTC ACG GAC CAG GCC ACG GTA GAG CGC TTT GGG AAG GAG CAC	450
Leu Phe Thr Asp Gln Ala Thr Val Glu Arg Phe Gly Lys Glu His	
75 80 85	
GCA GTC ATC ATC CTC AAC CAC AAC TTC GAG ATC GAC TTC CTC TGT	495
Ala Val Ile Ile Leu Asn His Asn Phe Glu Ile Asp Phe Leu Cys	
90 95 100	
GGG TGG ACC ATG TGT GAG CGC TTC GGA GTG CTG GGG AGC TCC AAG	540
Gly Trp Thr Met Cys Glu Arg Phe Gly Val Leu Gly Ser Ser Lys	
105 110 115	
GTC CTC GCT AAG AAG GAG CTG CTC TAC GTG CCC CTC ATC GGC TGG	585
Val Leu Ala Lys Lys Glu Leu Leu Tyr Val Pro Leu Ile Gly Trp	
120 125 130	
ACG TGG TAC TTT CTG GAG ATT GTG TTC TGC AAG CGG AAG TGG GAG	630
Thr Trp Tyr Phe Leu Glu Ile Val Phe Cys Lys Arg Lys Trp Glu	
135 140 145	
GAG GAC CGG GAC ACC GTG GTC GAA GGG CTG AGG CGC CTG TCG GAC	675
Glu Asp Arg Asp Thr Val Val Glu Gly Leu Arg Arg Leu Ser Asp	
150 155 160	
TAC CCC GAG TAC ATG TGG TTT CTC CTG TAC TGC GAG GGG ACG CGC	720
Tyr Pro Glu Tyr Met Trp Phe Leu Leu Tyr Cys Glu Gly Thr Arg	
165 170 175	
TTC ACG GAG ACC AAG CAC CGC GTT AGC ATG GAG GTG GCG GCT GCT	765
Phe Thr Glu Thr Lys His Arg Val Ser Met Glu Val Ala Ala Ala	
180 185 190	
AAG GGG CTT CCT GTC CTC AAG TAC CAC CTG CTG CCG CGG ACC AAG	810
Lys Gly Leu Pro Val Leu Lys Tyr His Leu Leu Pro Arg Thr Lys	
195 200 205	
GGC TTC ACC ACC GCA GTC AAG TGC CTC CGG GGG ACA GTC GCA GCT	855
Gly Phe Thr Thr Ala Val Lys Cys Leu Arg Gly Thr Val Ala Ala	
210 215 220	
GTC TAT GAT GTA ACC CTG AAC TTC AGA GGA AAC AAG AAC CCG TCC	900
Val Tyr Asp Val Thr Leu Asn Phe Arg Gly Asn Lys Asn Pro Ser	
225 230 235	
CTG CTG GGG ATC CTC TAC GGG AAG AAG TAC GAG GCG GAC ATG TGC	945
Leu Leu Gly Ile Leu Tyr Gly Lys Lys Tyr Glu Ala Asp Met Cys	
240 245 250	
GTG AGG AGA TTT CCT CTG GAA GAC ATC CCG CTG GAT GAA AAG GAA	990
Val Arg Arg Phe Pro Leu Glu Asp Ile Pro Leu Asp Glu Lys Glu	
255 260 265	
GCA GCT CAG TGG CTT CAT AAA CTG TAC CAG GAG AAG GAC GCG CTC	1035

Inventors: David W. LEUNG et al.
Docket No.: 077319-0383

[illegible]

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ACYLTRANSFERASE

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Docket No.: 077319-0383

Figure 10 Translated sequence of LPAAT- γ 2 cDNA

CACGCTGGCGCTCTGGCCGGTCAGCAAGCAGCTCTACCGCCGCCCTCAACTGCCGCCTCGCC	61
TACTCACTCTGGAGCCTAGCACAAAAGTAGAAGCAACCCCAAGCACCTGTCACTGGAGACT	121
AATTATGCGGCACCCATACAGGGACCCCTCTGCGGCCATCATGGAGAGCCTTCATCTTGCC	181
CGTACAGTTTAAAGCGAAAAAGGAAGTATACAACAAAGTCCATAACTGGTC ATG CTG	238
	Met Leu
CTG GAG TGG TGG TCC TGC ACG GAG TGT ACA CTG TTC ACG GAC CAG	283
Leu Glu Trp Trp Ser Cys Thr Glu Cys Thr Leu Phe Thr Asp Gln	
5 10 15	
GCC ACG GTA GAG CGC TTT GGG AAG GAG CAC GCA GTC ATC ATC CTC	328
Ala Thr Val Glu Arg Phe Gly Lys Glu His Ala Val Ile Ile Leu	
20 25 30	
AAC CAC AAC TTC GAG ATC GAC TTC CTC TGT GGG TGG ACC ATG TGT	373
Asn His Asn Phe Glu Ile Asp Phe Leu Cys Gly Trp Thr Met Cys	
35 40 45	
GAG CGC TTC GGA GTG CTG GGG AGC TCC AAG GTC CTC GCT AAG AAG	418
Glu Arg Phe Gly Val Leu Gly Ser Ser Lys Val Leu Ala Lys Lys	
50 55 60	
GAG CTG CTC TAC GTG CCC CTC ATC GGC TGG ACG TGG TAC TTT CTG	463
Glu Leu Leu Tyr Val Pro Leu Ile Gly Trp Thr Trp Tyr Phe Leu	
65 70 75	
GAG ATT GTG TTC TGC AAG CGG AAG TGG GAG GAG GAC CGG GAC ACC	508
Glu Ile Val Phe Cys Lys Arg Lys Trp Glu Glu Asp Arg Asp Thr	
80 85 90	
GTG GTC GAA GGG CTG AGG CGC CTG TCG GAC TAC CCC GAG TAC ATG	553
Val Val Glu Gly Leu Arg Arg Leu Ser Asp Tyr Pro Glu Tyr Met	
95 100 105	
TGG TTT CTC CTG TAC TGC GAG GGG ACG CGC TTC ACG GAG ACC AAG	598
Trp Phe Leu Leu Tyr Cys Glu Gly Thr Arg Phe Thr Glu Thr Lys	
110 115 120	
CAC CGC GTT AGC ATG GAG GTG GCG GCT GCT AAG GGG CTT CCT GTC	643
His Arg Val Ser Met Glu Val Ala Ala Ala Lys Gly Leu Pro Val	
125 130 135	
CTC AAG TAC CAC CTG CTG CCG CGG ACC AAG GGC TTC ACC ACC GCA	688
Leu Lys Tyr His Leu Leu Pro Arg Thr Lys Gly Phe Thr Thr Ala	
140 145 150	
GTC AAG TGC CTC CGG GGG ACA GTC GCA GCT GTC TAT GAT GTA ACC	733
Val Lys Cys Leu Arg Gly Thr Val Ala Ala Val Tyr Asp Val Thr	
155 160 165	
CTG AAC TTC AGA GGA AAC AAG AAC CCG TCC CTG CTG GGG ATC CTC	778
Leu Asn Phe Arg Gly Asn Lys Asn Pro Ser Leu Leu Gly Ile Leu	
170 175 180	
TAC GGG AAG AAG TAC GAG GCG GAC ATG TGC GTG AGG AGA TTT CCT	823
Tyr Gly Lys Lys Tyr Glu Ala Asp Met Cys Val Arg Arg Phe Pro	
185 190 195	
CTG GAA GAC ATC CCG CTG GAT GAA AAG GAA GCA GCT CAG TGG CTT	868
Leu Glu Asp Ile Pro Leu Asp Glu Lys Glu Ala Ala Gln Trp Leu	
200 205 210	
CAT AAA CTG TAC CAG GAG AAG GAC GCG CTC CAG GAG ATA TAT AAT	913
His Lys Leu Tyr Gln Glu Lys Asp Ala Leu Gln Glu Ile Tyr Asn	
215 220 225	
CAG AAG GGC ATG TTT CCA GGG GAG CAG TTT AAG CCT GCC CGG AGG	958
Gln Lys Gly Met Phe Pro Gly Glu Gln Phe Lys Pro Ala Arg Arg	
230 235 240	
CCG TGG ACC CTC CTG AAC TTC CTG TCC TGG GCC ACC ATT CTC CTG	1003
Pro Trp Thr Leu Leu Asn Phe Leu Ser Trp Ala Thr Ile Leu Leu	
245 250 255	
TCT CCC CTC TTC AGT TTT GTC TTG GGC GTC TTT GCC AGC GGA TCA	1048
Ser Pro Leu Phe Ser Phe Val Leu Gly Val Phe Ala Ser Gly Ser	

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Figure 10 (continued)

260	265	270	
CCT CTC CTG ATC CTG ACT TTC TTG GGG TTT GTG GGA GCA GCT TCC			1093
Pro Leu Leu Ile Leu Thr Phe Leu Gly Phe Val Gly Ala Ala Ser			
275	280	285	
TTT GGA GTT CGC AGA CTG ATA GGA GTA ACT GAG ATA GAA AAA GGC			1138
Phe Gly Val Arg Arg Leu Ile Gly Val Thr Glu Ile Glu Lys Gly			
290	295	300	
TCC AGC TAC GGA AAC CAA GAG TTT AAG AAA AAG GAA TAA TTAATGGC			1185
Ser Ser Tyr Gly Asn Gln Glu Phe Lys Lys Lys Glu ***			
305	310		
TGTGACTGAACACACGCGGCCCTGACGGTGGTATCCAGTTAACTCAAAACCAACACACAG			1245
AGTGCAGGAAAAGACAATTAGAACTATTTTTCTTATTAAGTGGTGACTAATATTAACAA			1305
AACTTGAGCCAAGAGTAAAGAATTCAGAAGGCCTGTCAGGTGAAGTCTTCAGCCTCCCAC			1365
AGCGCAGGGTCCCAGCATCTCCACGCGCGCCCGTGGGAGGTGGGTCCGGCCGGAGAGGCC			1425
TCCCGCGGACGCCGTCTCTCCAGAACTCCGCTTCCAAGAGGGACCTTTGGCTGCTTTCTC			1485
TCCTTAACTTAGATCAAATTTTAAAAAAAAAAAAAAAAA			1523

TGA	AACCCAGCGGCTC	CATCTCAGCTTCTGGTTTC	TAA	GTC	CA	TGTGCCA	AAAGGCTGCCAG		61
GAAGGAGACGCCTT	CCTGAGTCCTGGATCTT	CTTCTTCTTGAAATCTTTGACTGTGGG						121	
TAGTTATT	TATTTCTGAATAAGAGCGTCCACGCATC		Met	Asp	Leu	Ala	Gly Leu	175	
							5		
CTG AAG TCT CAG TTC CTG TGC CAC CTG GTC TTC TGC TAC GTC TTT								220	
Leu Lys Ser Gln Phe Leu Cys His Leu Val Phe Cys Tyr Val Phe									
	10		15				20		
ATT GCC TCA GGG CTA ATC ATC AAC ACC ATT CAG CTC TTC ACT CTC								265	
Ile Ala Ser Gly Leu Ile Ile Asn Thr Ile Gl n Leu Phe Thr Leu									
	25		30				35		
CTC CTC TGG CCC ATT AAC AAG CAG CTC TTC CGG AAG ATC AAC TGC								310	
Leu Leu Trp Pro Ile Asn Lys Gl n Leu Phe Arg Lys Ile Asn Cys									
	40		45				50		
AGA CTG TCC TAT TGC ATC TCA AGC CAG CTG GTG ATG CTG CTG GAG								355	
Arg Leu Ser Tyr Cys Ile Ser Ser Gl n Leu Val Met Leu Leu Gl u									
	55		60				65		
TGG TGG TCG GGC ACG GAA TGC ACC ATC TTC ACG GAC CCG CGC GCC								400	
Trp Trp Ser Gly Thr Gl u Cys Thr Ile Phe Thr Asp Pro Arg Ala									
	70		75				80		
TAC CTC AAG TAT GGG AAG GAA AAT GCC ATC GTG GTT CTC AAC CAC								445	
Tyr Leu Lys Tyr Gly Lys Gl u Asn Ala Ile Val Val Leu Asn His									
	85		90				95		
AAG TTT GAA ATT GAC TTT CTG TGT GGC TGG AGC CTG TCC GAA CGC								490	
Lys Phe Gl u Ile Asp Phe Leu Cys Gly Trp Ser Leu Ser Gl u Arg									
	100		105				110		
TTT GGG CTG TTA GGG GGC TCC AAG GTC CTG GCC AAG AAA GAG CTG								535	
Phe Gly Leu Leu Gly Gly Ser Lys Val Leu Ala Lys Lys Gl u Leu									
	115		120				125		
GCC TAT GTC CCA ATT ATC GGC TGG ATG TGG TAC TTC ACC GAG ATG								580	
Ala Tyr Val Pro Ile Ile Gly Trp Met Trp Tyr Phe Thr Gl u Met									
	130		135				140		
GTC TTC TGT TCG CGC AAG TGG GAG CAG GAT CGC AAG ACG GTT GCC								625	
Val Phe Cys Ser Arg Lys Trp Gl u Gl n Asp Arg Lys Thr Val Ala									
	145		150				155		
ACC AGT TTG CAG CAC CTC CGG GAC TAC CCC GAG AAG TAT TTT TTC								670	
Thr Ser Leu Gl n His Leu Arg Asp Tyr Pro Gl u Lys Tyr Phe Phe									
	160		165				170		
CTG ATT CAC TGT GAG GGC ACA CGG TTC ACG GAG AAG AAG CAT GAG								715	
Leu Ile His Cys Gl u Gly Thr Arg Phe Thr Gl u Lys Lys His Gl u									
	175		180				185		
ATC AGC ATG CAG GTG GCC CGG GCC AAG GGG CTG CCT CGC CTC AAG								760	
Ile Ser Met Gl n Val Ala Arg Ala Lys Gly Leu Pro Arg Leu Lys									
	190		195				200		
CAT CAC CTG TTG CCA CGA ACC AAG GGC TTC GCC ATC ACC GTG AGG								805	
His His Leu Leu Pro Arg Thr Lys Gly Phe Ala Ile Thr Val Arg									
	205		210				215		
AGC TTG AGA AAT GTA GTT TCA GCT GTA TAT GAC TGT ACA CTC AAT								850	
Ser Leu Arg Asn Val Val Ser Ala Val Tyr Asp Cys Thr Leu Asn									
	220		225				230		
TTC AGA AAT AAT GAA AAT CCA ACA CTG CTG GGA GTC CTA AAC GGA								895	
Phe Arg Asn Asn Gl u Asn Pro Thr Leu Leu Gly Val Leu Asn Gly									
	235		240				245		
AAG AAA TAC CAT GCA GAT TTG TAT GTT AGG AGG ATC CCA CTG GAA								940	
Lys Lys Tyr His Ala Asp Leu Tyr Val Arg Arg Ile Pro Leu Gl u									
	250		255				260		
GAC ATC CCT GAA GAC GAT GAC GAG TGC TCG GCC TGG CTG CAC AAG								985	
Asp Ile Pro Gl u Asp Asp Asp Gl u Ser Ala Trp Leu His Lys									
	265		270				275		

Inventors: David W. LEUNG et al.
Docket No.: 077319-0383

[illegible]

Title: METHOD OF SCREENING
COMPOUNDS THAT INHIBIT
LYSOPHOSPHATIDIC ACID
ACYLTRANSFERASE
Inventors: David W. LEUNG et al.
Docket No.: 077319-0383

Figure 12

	10	20	30	40	50
LPAAT-γ1	MGLLAFLKTQ	FVLHLLVGFV	FVVSGLVINF	VQ-LCTLALW	PVSKQLYRRL
LPAAT-γ2	-----	-----	-----	-----	-----
LPAAT-δ	MDLAGLLKSQ	FLCHLVFCYV	FIASGLIINT	IQ-LFTLLLW	PINKQLFRKI
	60	70	80	90	100
LPAAT-γ1	NCRLAYSLWS	QLVMLLEWWS	CTECTLFSTDQ	ATVERFGKEH	AVIILNHNFE
LPAAT-γ2	-----	---MLLEWWS	CTECTLFSTDQ	ATVERFGKEH	AVIILNHNFE
LPAAT-δ	NCRLSYCISS	QLVMLLEWWS	GTECTIFTDP	RAYLKYGKEN	AIVVLNHNFE
	110	120	130	140	150
LPAAT-γ1	IDFLCGWTMC	ERFGVLGSSK	VLAKKELLYV	PLIGWTWYFL	EIVFCKRKWE
LPAAT-γ2	IDFLCGWTMC	ERFGVLGSSK	VLAKKELLYV	PLIGWTWYFL	EIVFCKRKWE
LPAAT-δ	IDFLCGWSHS	ERFGVLGSSK	VLAKKELLYV	PIIGWMWYFT	EMVFCRSRWE
	160	170	180	190	200
LPAAT-γ1	EDRDTVVEGL	RRLSDYPEYM	WFLLYCEGTR	FTETKHRVSM	EVAAAKGLPV
LPAAT-γ2	EDRDTVVEGL	RRLSDYPEYM	WFLLYCEGTR	FTETKHRVSM	EVAAAKGLPV
LPAAT-δ	QDRKTVATSL	QHLRDYPEKY	FFLIHCEGTR	FTEKKHEISM	QVARAKGLPR
	210	220	230	240	250
LPAAT-γ1	LKYHLLPRTK	GFTTAVKCLR	GTVAAYVDVT	LNF-RGNKNP	SLLGILYGKK
LPAAT-γ2	LKYHLLPRTK	GFTTAVKCLR	GTVAAYVDVT	LNF-RGNKNP	SLLGILYGKK
LPAAT-δ	LKHLLPRTK	GFAITVRSLR	NVSAVYDCT	LNF-RNNENP	LLGLVNGKK
	260	270	280	290	300
LPAAT-γ1	YEADMCVRRF	PLEDIPLEK	EAAQWLHKLY	QEKDALQEIY	NQKGMFPGEQ
LPAAT-γ2	YEADMCVRRF	PLEDIPLEK	EAAQWLHKLY	QEKDALQEIY	NQKGMFPGEQ
LPAAT-δ	YHADLYVRR	PLEDIPEDD	EC ³ AWLHKLY	QEKDAFQEEY	YRTGTFPETP
	310	320	330	340	350
LPAAT-γ1	FKPARRPWT	LNFLSWATIL	LSPLFSFVLG	VFASGSPLLI	---LTFLGFV
LPAAT-γ2	FKPARRPWT	LNFLSWATIL	LSPLFSFVLG	VFASGSPLLI	---LTFLGFV
LPAAT-δ	MVPPRRPWT	VNWLFWASLV	LYPFFQFLVS	MIRSGSSLTL	---ASFILVF
	360	370	380		
LPAAT-γ1	GAASFGVRR	IGVTEIEKGS	SYGNQEF--K	KKE*	
LPAAT-γ2	GAASFGVRR	IGVTEIEKGS	SYGNQEF--K	KKE*	
LPAAT-δ	FVASVGVRW	IGVTEIDKGS	AYGNSDSKQK	LND*	

Title: METHOD OF SCREENING
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LYSOPHOSPHATIDIC ACID
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Docket No.: 077319-0383

Figure 13

